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RAW SEQUENCE LISTING

DATE: 09/24/2002

PATENT APPLICATION: US/10/092,947

TIME: 11:16:09

Input Set : N:\Crf4\09232002\J092947.raw

Output Set: N:\CRF4\09242002\J092947.raw

1 <110> APPLICANT: WOLFF, Anne M
 2 APPEL, Karen F
 3 PETERSEN, Jesper F
 4 POULSEN, Ulla
 5 ARNAU, Jose
 6 JACOBSEN, Mette D
 7 <120> TITLE OF INVENTION: MUCOR RECOMBINANT GENE EXPRESSION
 8 <130> FILE REFERENCE: WOLFF=3
 9 <140> CURRENT APPLICATION NUMBER: US/10/092,947
 10 <141> CURRENT FILING DATE: 2002-03-08
 11 <150> PRIOR APPLICATION NUMBER: US 60/274,650
 12 <151> PRIOR FILING DATE: 2001-03-12
 13 <160> NUMBER OF SEQ ID NOS: 65
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 2525
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Mucor circinelloides
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 22 <222> LOCATION: (542)..(724)
 23 <223> OTHER INFORMATION: Exon of pkar
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 42 <222> LOCATION: (1708)..(1760)
 43 <223> OTHER INFORMATION: Intron of pkar
 44 <400> SEQUENCE: 1

Does Not Comply
Corrected Diskette Needed

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45	aagctttatt catttcactg gtcaacgtaa gtacatttct ctcagtattg gtcgctttta	60
46	tatcatcttt ttggctgctt tacgtgatga acaaaacatt atgctactaa acccagctca	120
47	gtttgagata ttcggtgaaa gaaactattt ccataactga aaaagttaaa ccaaaaagat	180
48	atatgaaaat gatacattta cttgttcatt tgagctccat attaatactc ttctcctcta	240
49	gttggcatgt ctttttgcaa gccaaagcta cctatagctc aggtctatta gatgtatcat	300
50	cttgatcttt ttggaattga ataaataaat ttcttgatt ttaaaatgta acactttaat	360
51	gcctaatttc tgcgtgcaat gtcgtttttt ttctgtgat aacctgaac tgctcaaag	420
52	ctttcatgat gtcactcat aatctgttg gttacatcca atactgttaa attgtatgtg	480
53	ttgatcttga gtataaggga tcgatcattt gattgtcttt ttctcctcta ttttcattaa	540
54	a atg atc act gac gaa cat ccg ttt gaa ttt gcg cct cag caa gat gaa	589
55	Met Ile Thr Asp Glu His Pro Phe Glu Phe Ala Pro Gln Gln Asp Glu	
56	1 5 10 15	
57	tac acg cag ctg ttg aca gag tta cat aac gaa tac tgc gct gag caa	637
58	Tyr Thr Gln Leu Leu Thr Glu Leu His Asn Glu Tyr Cys Ala Glu Gln	
59	20 25 30	
60	cca cta gat gtg ctt cag ttc tgc tcc aac ttt ttc att cgc aaa ctc	685
61	Pro Leu Asp Val Leu Gln Phe Cys Ser Asn Phe Phe Ile Arg Lys Leu	
62	35 40 45	
63	gaa gag cag cgc ttg gag cat aga aac aac cac cat tcc cgtaacaact	734
64	Glu Glu Gln Arg Leu Glu His Arg Asn Asn His His Ser	
65	50 55 60	
66	tgtttgatag taaagtgtct ctgccacgag cctagtgatg gatgctaacg tttttcctta	794
W--> 67	g ccn aat gat acc agt aat gat tta cat cct ttg tgt gag caa cca caa	843
68	Pro Asn Asp Thr Ser Asn Asp Leu His Pro Leu Cys Glu Gln Pro Gln	
69	65 70 75	
70	gaa gac ttt tca caa cag caa ggc atc cag tgg gaa acc acg cat atg	891
71	Glu Asp Phe Ser Gln Gln Gln Gly Ile Gln Trp Glu Thr Thr His Met	
72	80 85 90	
73	ggc cat ccc aac gac cac ggt gct ctt cat gat gat gat gat gat ccg	939
74	Gly His Pro Asn Asp His Gly Ala Leu His Asp Asp Asp Asp Asp Pro	
75	95 100 105	
76	ttg gaa gac gaa gac gat gaa gag ttt gac aaa ttt tca act gaa cct	987
77	Leu Glu Asp Glu Asp Asp Glu Glu Phe Asp Lys Phe Ser Thr Glu Pro	
78	110 115 120 125	
79	ttg ccc tcg ctg cct ccc aca aac tat aac cgt ggc cgc cgc aca tct	1035
80	Leu Pro Ser Leu Pro Pro Thr Asn Tyr Asn Arg Gly Arg Arg Thr Ser	
81	130 135 140	
82	gtt aag tgc aga gag cat ggc acc cag cgc caa cca aga ctt tgt caa	1083
83	Val Lys Cys Arg Glu His Gly Thr Gln Arg Gln Pro Arg Leu Cys Gln	
84	145 150 155	
85	ggc cat cat ccc caa atc tca ggc aca agc gag cgc atc aaa gtc tcc	1131
86	Gly His His Pro Gln Ile Ser Gly Thr Ser Glu Arg Ile Lys Val Ser	
87	160 165 170	
88	atc agc aac aac ttt ttg ttt cgc aac ctg gac gaa gag cag tac ctg	1179
89	Ile Ser Asn Asn Phe Leu Phe Arg Asn Leu Asp Glu Glu Gln Tyr Leu	
90	175 180 185	
91	gat gtg gtg aat gcc atg tct gaa aag cgc gtc gtc aag ggc acc aca	1227
92	Asp Val Val Asn Ala Met Ser Glu Lys Arg Val Val Lys Gly Thr Thr	
93	190 195 200 205	

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94	gtg atc gag caa ggc agt gtg ggt gat ttc ttc tac gtc gtc gag tcg	1275
95	Val Ile Glu Gln Gly Ser Val Gly Asp Phe Phe Tyr Val Val Glu Ser	
96	210 215 220	
97	ggt act ttg gat tgt ttt att ggg caa aac aag gtt acc aac tat gag	1323
98	Gly Thr Leu Asp Cys Phe Ile Gly Gln Asn Lys Val Thr Asn Tyr Glu	
99	225 230 235	
100	gca ggt ggt agc ttc ggt gaa tta gcc tta atg tac aac gcc cct cgt	1371
101	Ala Gly Gly Ser Phe Gly Glu Leu Ala Leu Met Tyr Asn Ala Pro Arg	
102	240 245 250	
103	gct gct act att att aca aca tca gac tct gtg ctt tgg gct ctg gac	1419
104	Ala Ala Thr Ile Ile Thr Thr Ser Asp Ser Val Leu Trp Ala Leu Asp	
105	255 260 265	
106	aga aac act tcg gca cca tcc ttg atg gag aac acc tca cgc aaa aga	1467
107	Arg Asn Thr Ser Ala Pro Ser Leu Met Glu Asn Thr Ser Arg Lys Arg	
108	270 275 280 285	
109	cgc atg tat gaa tac ttc tta tca gaa gtc gtc ttg tta aaa tcc ctg	1515
110	Arg Met Tyr Glu Tyr Phe Leu Ser Glu Val Val Leu Leu Lys Ser Leu	
111	290 295 300	
112	gaa tca tat gaa cag cat aaa att gcg gat gcc ctc gaa tca gtt tat	1563
113	Glu Ser Tyr Glu Gln His Lys Ile Ala Asp Ala Leu Glu Ser Val Tyr	
114	305 310 315	
115	ttt gaa gat gga cag gag gtt gtg aag cag ggt gat gtc gga gat cag	1611
116	Phe Glu Asp Gly Gln Glu Val Val Lys Gln Gly Asp Val Gly Asp Gln	
117	320 325 330	
118	ttc tac atc att gaa tcc ggt gaa gcc atc gtc ctg aag gaa gag aac	1659
119	Phe Tyr Ile Ile Glu Ser Gly Glu Ala Ile Val Leu Lys Glu Glu Asn	
120	335 340 345	
121	ggc gtc cag caa cag gtg aac cag ctt gag cga gga tcc tac ttt gga	1707
122	Gly Val Gln Gln Gln Val Asn Gln Leu Glu Arg Gly Ser Tyr Phe Gly	
123	350 355 360 365	
124	ggtaagatgg agcttggtgg ggttggtgat gtgtcgctaa ccactgtgtg ata gaa	1763
125	Glu	
126	ctg gcc ctg tta aac gat gct cct cga gct gca acc gta gtt gct cac	1811
127	Leu Ala Leu Leu Asn Asp Ala Pro Arg Ala Ala Thr Val Val Ala His	
128	370 375 380	
129	ggc aga ctc aag tgc gct aca ctg ggc aaa aag gca ttc act cgt ctt	1859
130	Gly Arg Leu Lys Cys Ala Thr Leu Gly Lys Lys Ala Phe Thr Arg Leu	
131	385 390 395	
132	ctt ggc cct gtt ttg gac atc ttg aag cgt aat tca gaa aac tat cat	1907
133	Leu Gly Pro Val Leu Asp Ile Leu Lys Arg Asn Ser Glu Asn Tyr His	
134	400 405 410	
135	gct gtc att aac cag caa tca taatcgacc aaaaagttac actagatttc	1958
136	Ala Val Ile Asn Gln Gln Ser	
137	415 420	
138	aaataaaaac catggatact ttccgatctg atgttgactt gactgtaaca aagcgacagg	2018
139	aaaaagaaac ttgatttgct tcctgaccaa caatgcagcc aatctcctta aacaagatgc	2078
140	tctctatttc ggctgaaaa tataacctcc ttgatttcgt attttgktgt tgtgcttttt	2138
141	tcctctcttc tctctctctc ttttctactct tgttataaaa aaaatatgac gggtatgatt	2198
142	cacagtatgg agagcaaccc ttgatgagcc tccacctcaa agcgccagcg gcctcttcta	2258

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145      gaccaggtaa ctgaattttg cttagggtgaa tcgggtgtcg gaaaaacaac ctttgtaaac      2438
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161      20              25              30
162      Pro Leu Asp Val Leu Gln Phe Cys Ser Asn Phe Phe Ile Arg Lys Leu
163      35              40              45
164      Glu Glu Gln Arg Leu Glu His Arg Asn Asn His His Ser Pro Asn Asp
165      50              55              60
166      Thr Ser Asn Asp Leu His Pro Leu Cys Glu Gln Pro Gln Glu Asp Phe
167      65              70              75              80
168      Ser Gln Gln Gln Gly Ile Gln Trp Glu Thr His Met Gly His Pro
169      85              90              95
170      Asn Asp His Gly Ala Leu His Asp Asp Asp Asp Asp Pro Leu Glu Asp
171      100             105             110
172      Glu Asp Asp Glu Glu Phe Asp Lys Phe Ser Thr Glu Pro Leu Pro Ser
173      115             120             125
174      Leu Pro Pro Thr Asn Tyr Asn Arg Gly Arg Arg Thr Ser Val Lys Cys
175      130             135             140
176      Arg Glu His Gly Thr Gln Arg Gln Pro Arg Leu Cys Gln Gly His His
177      145             150             155             160
178      Pro Gln Ile Ser Gly Thr Ser Glu Arg Ile Lys Val Ser Ile Ser Asn
179      165             170             175
180      Asn Phe Leu Phe Arg Asn Leu Asp Glu Glu Gln Tyr Leu Asp Val Val
181      180             185             190
182      Asn Ala Met Ser Glu Lys Arg Val Val Lys Gly Thr Thr Val Ile Glu
183      195             200             205
184      Gln Gly Ser Val Gly Asp Phe Tyr Val Val Glu Ser Gly Thr Leu
185      210             215             220
186      Asp Cys Phe Ile Gly Gln Asn Lys Val Thr Asn Tyr Glu Ala Gly Gly
187      225             230             235             240
188      Ser Phe Gly Glu Leu Ala Leu Met Tyr Asn Ala Pro Arg Ala Ala Thr
189      245             250             255
190      Ile Ile Thr Thr Ser Asp Ser Val Leu Trp Ala Leu Asp Arg Asn Thr
191      260             265             270
192      Ser Ala Pro Ser Leu Met Glu Asn Thr Ser Arg Lys Arg Arg Met Tyr

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*delete - "n" is only shown
in a nucleotide*

sequence

*Please
delete
any
similar
errors
in subsequent
sequences*

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TIME: 11:16:09

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196    Glu Gln His Lys Ile Ala Asp Ala Leu Glu Ser Val Tyr Phe Glu Asp
197    305          310          315          320
198    Gly Gln Glu Val Val Lys Gln Gly Asp Val Gly Asp Gln Phe Tyr Ile
199          325          330          335
200    Ile Glu Ser Gly Glu Ala Ile Val Leu Lys Glu Glu Asn Gly Val Gln
201          340          345          350
202    Gln Gln Val Asn Gln Leu Glu Arg Gly Ser Tyr Phe Gly Glu Leu Ala
203          355          360          365
204    Leu Leu Asn Asp Ala Pro Arg Ala Ala Thr Val Val Ala His Gly Arg
205          370          375          380
206    Leu Lys Cys Ala Thr Leu Gly Lys Lys Ala Phe Thr Arg Leu Leu Gly
207    385          390          395          400
208    Pro Val Leu Asp Ile Leu Lys Arg Asn Ser Glu Asn Tyr His Ala Val
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240    1          5          10          15
241    tcg cct tca tct caa aca arn atg gac gat ttt gaa atc aaa cag cca      96
242    Ser Pro Ser Ser Gln Thr Xaa Met Asp Asp Phe Glu Ile Lys Gln Pro

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